Amendments to the Specification

Please replace the title on page 1 of the specification as follows:

~~DESCRIPTION~~

~~Protein involved in restoration of cytoplasmic male sterility to fertility and gene encoding the protein and gene.~~

PROTEIN INVOLVED IN RESTORATION OF CYTOPLASMIC MALE STERILITY TO FERTILITY AND GENE ENCODING THE PROTEIN

Please replace the first paragraph of the specification on page 1 as follows:

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a Continuation-in-Part of United States Application No. 10/451,366, filed April 24, 2002, now abandoned, which is a National Stage of International Application No. *PCT/JP02/04092,* filed April 24, 2002, which was not filed in English under PCT Article 21(1), ~~and which claims priority of Japanese Application Nos.2001-128008,~~ and which claims priority of Japanese Application Nos.2001-128008, filed April 25, 2001, 2001-202082, filed July 3, 2001, and 2002-20083, filed January 29, 2002. The ~~disclosures~~ disclosure of each of these applications is incorporated by reference herein in ~~their entireties~~ its entirety.

Please replace the paragraph beginning "Technical Field" on page 1 as follows:

BACKGROUND OF THE INVENTION

Technical Field

The present invention relates to a gene involved in restoration from cytoplasmic male sterility to fertility. More specifically, the present invention relates to the gene involved ~~in restoration of cytoplasmic male sterility character~~ in restoration of cytoplasmic male sterility character (hereafter may be abbreviated to cms) used for developing a cultivar of a first filial hybrid (hereafter abbreviated to FI), and a vector and a transformant containing the gene.

To facilitate amendment of pages 1 and 1A, Applicants provide replacement pages 1 and 1A for the convenience of the Office.

Please replace the paragraph that begins with "In the present specification, . . ." on page 12 of the specification with the following amended paragraph:

In the present specification, the PPR motif is the "pentatricopeptide repeat" motif. This PPR motif is a motif structure of a novel protein found in the course of an Arabidopsis genome project. The base motif thereof is that a sequence of 35 degenerated amino acids is repeated in tandem on a primary structure of the protein. The PPR motif has the sequence represented by amino terminal (N terminal) ~~"VTYNTLISGYCKNGKLEEALELFEEMKEKGIKPDV"~~ "VTYNTLISGYCKNGKLEEALELFEEMKEKGIKPDV"-carboxyl terminal (C terminal) as a consensus amino acid sequence. This motif is ~~the~~ that proposed by Small and Peeters (reference: Trends Biochem. Sci. 2000, 25 46-47). In the year of the publication of the reference, about 200 genes capable of having this motif in the Arabidopsis genome were registered to a gene bank such as GenBank (http://www.ncbi.nlm.nih.gov/GenBank/index.html.) At present, possibility of presence of this motif structure in a certain protein can be easily determined by a program stored in Protein Families Database of Alignments and HMNs (hereafter abbreviated to Pfam; http://www.sanger.ac.uk/Software/Pfam/search.shtml) located in Sanger Institute, U.K.

Please replace the last paragraph that begins with "As the material for the measurement . . ." on page 23 of the specification with the following amended paragraph:

As the material for the measurement of the genetic distance of the DNA marker from the *Rf* gene, for example, there can be used ~~F~~$_2$ F_2 population of some thousand individuals which is obtained by self pollination of the radish F_1 generation produced by crossing of Kosena radish *(Raphanus sati vus* cv . Kosena) of the cms line with Yuanhong radish *(Raphanus sativus* cv. Yuanhong) of the *Rf* line according to the

method described in N. Koizuka et al. (~~Teor.~~ Theor. Appl. Genet. 100 :949-955, 2000). Analysis of these populations allows isolation of the DNA markers with a linkage in a form sandwiching the *Rf* gene and located in a position with a distance of about 0.2 cM from both sides thereof. By this step, the genome map as shown in Fig. 1, which shows the genetic distance of the marker from the *Rf* gene can be prepared.

Please replace the last paragraph that begins with "The homologues of the gene means . . ." on page 28 of the specification with the following amended paragraph:

The homologues of the gene means a series of related genes which have a sequence homology with the gene (or a gene product thereof) of the present invention and are recognized as a gene family on the basis of a similarity of a structural feature as described above and a biological function thereof ~~As~~ as described above. An allele of these ~~gene~~ genes is included.

Please replace the paragraph that begins with "Lambda clone CHI . . ." on page 58 of the specification with the following amended paragraph:

Lambda clone CHI (see Fig. 2, Cloned fragment of length of about 17 kb) carrying enough of the nucleotide sequence of SEQ ~~10~~ ID NO.1 was cleaved with a restriction enzyme *NotI* (Takara) which is located in the multiple cloning site, and then separated from the vector by gel electrophoresis using agarose for collecting the fragment, and the collected fragment was cloned in the NotI site of the vector pBIGRZ2(Bioscience and Industry 55 (1997) 37-39) for plant transformation to prepare the vector CHI/pBIGRZ2 for plant transformation. The detail will be presented below.